

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 21, 2006, 13:52:27 ; Search time 25.2468 Seconds
(without alignments)
1303.914 Million cell updates/sec

Title: US-10-517-309-1_49T059_AND4
Perfect score: 379
Sequence: 1 DWKIQKGMIRPLEATSLNPV.....GSGVKNFKAGDKVAVLSHL 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	316	83.4	61	8	ADG93324 Adg93324 A thalian
2	316	83.4	324	3	AAG39983 Aag39983 Arabidops
3	316	83.4	329	3	AAG39982 Aag39982 Arabidops
4	316	83.4	329	5	ABB92914 Abb92914 Herbicida
5	316	83.4	329	8	ADG93321 Adg93321 Arabidops
6	316	83.4	329	8	ADJ63876 Adj63876 Plant lip
7	316	83.4	354	3	AAG39981 Aag39981 Arabidops
8	313	82.6	262	3	AAG05068 Aag05068 Arabidops
9	313	82.6	267	3	AAG05067 Aag05067 Arabidops
10	313	82.6	292	3	AAG05066 Aag05066 Arabidops
11	248	65.4	329	8	ADG93323 Adg93323 Spinacia
12	247	65.2	61	8	ADG93325 Adg93325 S olerace

XX
 PR 21-JUN-2002; 2002FR-00007729.
 XX
 PA (GENO-) GENOPLANTE-VALOR.
 XX
 PI Miras S, Salvi D, Rolland N, Joyard J, Ferro M, Garin J;
 PI Grunwald D;
 XX
 DR WPI; 2004-082507/08.
 XX
 PT New intraplastid targeting peptide, useful for delivering fused
 PT heterologous sequences for preparing transgenic plants having altered
 PT characteristics.
 XX
 PS Claim 1; SEQ ID NO 4; 63pp; French.
 XX
 CC This invention relates to a novel intraplastid targeting peptide. The
 CC peptide may be used to transport selected proteins to plasts,
 CC specifically chloroplasts, to create transgenic plants having altered
 CC characteristics. These altered characteristics include, for example,
 CC improved biosynthesis of lipids, starch, vitamins, hormones or proteins;
 CC increased resistance to diseases and herbicides; more efficient light
 CC capture; or overexpression of proteins involved in bioremediation. The
 CC invention does not depend on the TOC or TIC membrane import pathways, so
 CC does not compete with, or saturate, them, and importation into the
 CC internal chloroplast membrane is achieved without cleavage of the
 CC targeting peptide. The present sequence is that of a region the IE41
 CC protein of Arabidopsis thaliana which is related to the invention.
 XX
 SQ Sequence 61 AA;

Query Match 83.4%; Score 316; DB 8; Length 61;
 Best Local Similarity 100.0%; Pred. No. 1e-35;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LEATSLNPVDWKIQKGMIRPFLPRKFPCIPATDVAGEVVEVGSGVKNFKAGDKVVAVLSH 71
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 Qy 72 L 72
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 Db 61 L 61

RESULT 2
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 ID AAG39983 standard; protein; 324 AA.
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 AC AAG39983;
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 DT 18-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 49547.
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 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.

XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 83.4%; Score 316; DB 3; Length 324;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      72 L 72
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Db      95 L 95

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RESULT 3

AAG39982

ID AAG39982 standard; protein; 329 AA.

XX

AC AAG39982;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 49546.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX

OS *Arabidopsis thaliana*.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-00301439.

XX

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

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PR 08-APR-1999; 99US-0128714P.

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